

WIPER (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Msrch_un n.a. - n.a. database search, using Smith-Waterman algorithm

on: Thu Aug 21 10:35:24 1997; Maspar time 451.64 Seconds
929.139 Million cell updates/sec

Tabular output not generated.

Title: >US-08-469-637A-1
Description: (1-1527) from US08469637A.seq
Perfect Score: 1527
N.A. Sequence: 1 GCCCCAGCGCGCGCTCCAA.....TTCACGTGAGAAAAA 1527
Comp: GCGGGCTCGCGCGGAGGTT.....AAGTTGACCTTTTTTTT

Scoring table: TABLE default

Gap 6

Rmatch STD: Dbase 0; Query 0

Searched: 359085 seqs, 137405154 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STS-THREE
1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204
7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210
13:EST211 14:EST212 15:EST213 16:EST214 17:EST215
18:EST216 19:EST217 20:EST218 21:EST219 22:EST220
23:EST221 24:EST222 25:EST223 26:EST224 27:EST225
28:EST226 29:EST227 30:EST228 31:EST229 32:EST230
33:EST231 34:EST232 35:EST233 36:STS1 37:STS2 38:STS3
39:STS4 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
46:STS11 47:STS12 48:STS13
EST-STS-FOUR
49:ESTST1 50:ESTST2 51:ESTST3 52:ESTST4 53:ESTST5
54:ESTST6 55:ESTST7 56:ESTST8 57:ESTST9 58:ESTST10
59:ESTST11 60:ESTST12 61:ESTST13 62:ESTST14 63:ESTST15
64:ESTST16 65:ESTST17 66:ESTST18 67:ESTST19 68:ESTST20
69:ESTST21 70:ESTST22 71:ESTST23 72:ESTST24 73:ESTST25
74:ESTST26 75:ESTST27 76:ESTST28 77:ESTST29 78:ESTST30
79:ESTST31 80:ESTST32 81:ESTST33 82:ESTST34 83:ESTST35
84:ESTST36 85:ESTST37 86:ESTST38 87:ESTST39 88:ESTST40
89:ESTST41 90:ESTST42 91:ESTST43 92:ESTST44 93:ESTST45
94:ESTST46 95:ESTST47 96:ESTST48 97:ESTST49 98:ESTST50
99:ESTST51 100:ESTST52 101:ESTST53 102:ESTST54
103:ESTST55 104:ESTST56 105:ESTST57 106:ESTST58 107:ESTST59
108:ESTST60

Statistics: Mean 11.492; Variance 1.942; scale 5.918

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	461	30.2	463	65	AA233719	z17908.r1 Soares NIH	0.00e+00
2	461	30.2	463	83	HS1151638	z17908.r1 Soares NIH	0.00e+00
3	335	21.9	530	16	AA195113	z135a03.r1 Soares NIH	0.00e+00
4	335	21.9	530	54	AA195113	z135a03.r1 Soares NIH	0.00e+00
5	21	1.4	105	91	KM1135	ma42d03.r1 Soares mou	9.46e-03
6	21	1.4	107	98	NMAA17046	mp33f02.r1 Soares 2nb	9.46e-03
7	21	1.4	107	5	AA117046	mp33f02.r1 Soares 2nb	9.46e-03
8	21	1.4	156	36	DM36D75	D. melanogaster STS d	9.46e-03
9	21	1.4	194	48	HOMUT5145	Human STS UT5145.	9.46e-03
10	21	1.4	212	12	AA181616	zps2d02.r1 Stratagene	9.46e-03
11	22	1.4	241	77	AT48713	15616 Arabidopsis th	5.47e-04
12	22	1.4	245	40	G11923	human STS MR4116	9.46e-03
13	21	1.4	253	38	G06067	human STS WT-6405.	9.46e-03
14	22	1.4	267	95	NM5835	ma38f10.r1 Soares mou	5.47e-04
15	22	1.4	281	92	NM1157384	mv25d08.r1 GuayWoodfo	5.47e-04
16	22	1.4	281	70	AA239461	mv25d08.r1 GuayWoodfo	5.47e-04
17	21	1.4	312	42	G21574	human STS WT-13991	9.46e-03
18	22	1.4	343	59	AA124222	mp38c08.r1 Soares 2nb	5.47e-04
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20	22	1.4	351	36	DM122E45	D. melanogaster STS d	9.46e-03
21	21	1.4	377	90	NM05110	mb33902.r1 Soares mou	9.46e-03
22	21	1.4	380	60	AA142684	mg64e05.r1 Soares 2nb	9.46e-03
23	21	1.4	380	100	NMAA42684	mg64e05.r1 Soares 2nb	9.46e-03
24	21	1.4	392	53	T03759	1B862 Infant brain, B	9.46e-03
25	21	1.4	400	39	G10922	human STS SHC-13782	5.47e-04
26	22	1.4	412	70	AA222925	mv98c06.r1 GuayWoodfo	9.46e-03
27	21	1.4	422	67	AA241200	mv95h10.r1 Soares mou	9.46e-03
28	21	1.4	422	72	AA252560	zps7h05.r1 Stratagene	9.46e-03
29	21	1.4	427	76	AT3618	11139 Arabidopsis th	9.46e-03
30	21	1.4	431	21	AA219045	zq16e09.r1 Stratagene	9.46e-03
31	21	1.4	439	21	AA020160	mh49h05.r1 Soares mou	9.46e-03
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ALIGNMENTS

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LOCUS z17908.r1 Soares NIHMPu S1 Homo sapiens CDNA clone 666590 5'
DEFINITION AA233719
ACCESSION g1856711
NID KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 463)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 448.

FEATURES

Source

1..463

/organism="Homo sapiens"

/note="Organ: mixed (see below); Vector: p7773D-Pac

(Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 2NDHM, pregnant uterus

NbHPV, and fetal heart NBH19W) were mixed, and ss circles

were made in vitro. Following HAP purification, this DNA

was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from pools of

5,000 clones made from the same 3 libraries. The pools

consisted of T.M.A.G.E. clones 260232-265223,

340488-345479, and 484488-489479."

/clone="666590"

/clone_1lb="Soares NhMPV S1"

/tissue_type="Pooled human melanocyte, fetal heart, and

pregnant uterus"

/lab_host="DH10B"

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BASE COUNT 154 a 104 c 88 g 117 t

ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0.00e+00;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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61 ggcacaaagacaccccttgaaggcctgaatgacgcacactaaagcactaaagcact 120

1055 ggcacaaagacaccccttgaaggcctgaatgacgcacactaaagcactaaagcact 1114

121 tccccaaaacttcaactcagagtcctaaagaagacacacagctgtctctccacac 180

1115 ttcccaaaaacttcaactcagagtcctaaagaagacacacagctgtctctccacac 1174

181 tgtacaattgtatcagaagtatttttgaagtataagtaacagagtcacacagtaa 240

1175 tgtacaattgtatcagaagtatttttgaagtataagtaacagagtcacacagtaa 1234

241 aataaagctgtctataacttgaatgaaatggccattgacgtgttctccacaattggcgagatc 300

1235 aataaagctgtctataacttgaatgaaatggccattgacgtgttctccacaattggcgagatc 1294

301 ccattgagtgagcgaactgttctcagagccttgaggtcttcagtatatacttccacata 360

1295 ccattgagtgagcgaactgttctcagagccttgaggtcttcagtatatacttccacata 1354

361 ccagtgactaatatttggccacaggtactaaagaagacactatgtgtggagaaagagactaac 420

1355 ccagtgactaatatttggccacaggtactaaagaagacactatgtgtggagaaagagactaac 1414

421 atctcctccaataaaccacaatgttcaatccaactgtcagat 463

1415 atctcctccaataaaccacaatgttcaatccaactgtcagat 1457

RESULT 2

ID HS1151638 standard; RNA; EST; 463 BP.

AC AA233719;

NI 91856711

DT 06-MAR-1997 (Rel. 51, Created)

06-MAR-1997 (Rel. 51, last updated, Version 1)

DE zrt47g08.r1 Soares NhMPV S1 Homo sapiens cDNA clone 666590 5'.

KW EST.

OC Homo sapiens (human)

OC Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrate; Eutheria; Primates; Catarrhini; Homidae; Homo.

RN [1]

RP 1-463

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Maira M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevaakis E., Waterston R., Williamson A., Woldmann P., Wilson R.,

RT "The Mashu-Merck EST Project";

RU Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC estewatson.wustl.edu This clone is available royalty-free through

CC LNL; contact the IMAGE Consortium (info@image.jnl.gov) for

CC further information. Seq primer: -28m13 rev2 ET from Amersham High

CC quality sequence stop: 448.

Key Location/Qualifiers

FT source

FT 1..463

/organism="Homo sapiens"

/note="Organ: mixed (see below); Vector: p7773D-Pac

(Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 2NDHM, pregnant uterus

NbHPV, and fetal heart NBH19W) were mixed, and ss circles

were made in vitro. Following HAP purification, this DNA

was used as tracer in a subtractive hybridization reaction

FT clones made from the same 3 libraries. The pools consisted

FT of I.M.A.G.E. clones 260232-265223, 340488-345479, and

FT 484488-489479."

FT /clone="666590"

FT /clone_1lb="Soares NhMPV S1"

FT /tissue_type="Pooled human melanocyte, fetal heart, and

FT pregnant uterus"

FT /lab_host="DH10B"

FT <1..>463

FT mRNA

FT Sequence 463 BP, 154 A, 104 C, 88 G, 117 T, 0 other:

Query Match 30.2%; Score 461; DB 83; Length 463;

Best Local Similarity 99.8%; Pred. No. 0.00e+00;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 aggcattgcaaacaccagtcgacagatcctgaagctgctcagtttggcgataaaatg 60

995 aggcattgcaaacaccagtcgacagatcctgaagctgctcagtttggcgataaaatg 1054

61 ggcacaaagacaccccttgaaggcctgaatgacgcacactaaagcactaaagcact 120

1055 ggcacaaagacaccccttgaaggcctgaatgacgcacactaaagcactaaagcact 1114

121 tccccaaaacttcaactcagagtcctaaagaagacacacagctgtctctccacac 180

1115 ttcccaaaaacttcaactcagagtcctaaagaagacacacagctgtctctccacac 1174

181 tgtacaattgtatcagaagtatttttgaagtataagtaacagagtcacacagtaa 240

1175 tgtacaattgtatcagaagtatttttgaagtataagtaacagagtcacacagtaa 1234

241 aataaagctgtctataacttgaatgaaatggccattgacgtgttctccacaattggcgagatc 300

1235 aataaagctgtctataacttgaatgaaatggccattgacgtgttctccacaattggcgagatc 1294

301 ccattgagtgagcgaactgttctcagagccttgaggtcttcagtatatacttccacata 360

1295 ccattgagtgagcgaactgttctcagagccttgaggtcttcagtatatacttccacata 1354

Db 361 ccagtgactaatgttccacaggtactaaagaactatgtagtgagaaaggactaac 420
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QY 1355 CCAGTGACTAATTTTCCACAGGGTACTAAAGAACTGTATGTGGAGAAAGGACTAAC 1414
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Db 421 atctccccaataaacccaatggttaatccaactgtcagat 463
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QY 1415 ACTCTCTCCATAAACCCCAATGGTTATCCACACTGTAGAT 1457
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LOCUS AA195113 530 bp mRNA EST 17-JAN-1997
DEFINITION zr35a03.r1 Soares NHMPu SI Homo sapiens cDNA clone 665356 5',
ACCESSION AA195113
NID g1784803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 530)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
1..530
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHMU, and fetal heart NbHM19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
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/lab_host="DH10B"
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BASE COUNT 170 a 96 c 93 g 168 t 3 others
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Query Match 21.9%; Score 335; DB 16; Length 530;
Best Local Similarity 97.7%; Pred. No. 0.00e+00;
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 1178 ACAAAATGTATGAGAAAGTTATTTTGAATAATGATAGCTAACAGGCCAATCATCGTAAAAA 1237
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Db 61 taagctgctataactggaatgagccatgagctgtttcctcacaattgycgagatccca 120
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QY 1238 TAAGCTGCTTATTAACGGAATGCGCATGAGCTGTTCTCACAATTCGGCGAGATCCA 1297
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Db 121 tggatgagtaaacgtgtttctcaggccttgaggcttcagtgatatactttccatataca 180
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QY 1298 TGGATGAGTAACAGTGTTCCTCAGGCACTTAGAGCTTTCAGTGATATCTTCTCATTAACA 1357
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Db 181 gtgactaatlttgcacagaggtactaaagaactatgatgtaggagaaggactaacac 240
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ACCESSION AA195113
NID g1784803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 530)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
1..530
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHMU, and fetal heart NbHM19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/clone="665356"
/clone_lib="Soares NHMPu SI"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
MRNA
BASE COUNT 170 a 96 c 93 g 168 t 3 others
ORIGIN
Query Match 21.9%; Score 335; DB 54; Length 530;
Best Local Similarity 97.7%; Pred. No. 0.00e+00;
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 1 acaaatgtatcagaagttatttttagaataatgatagtaccaggtccaatcaaaaaa 60
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OY 1178 ACAATGTATCAGAGTATTTTGAATGATAGTACAGTCCAACTAGTAATAA 1237
DB 61 taagcgtcataactaactggaatgccaatgactgttctcccaattggcgatccca 120
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OY 1238 TAAGTCGCTTATTAACGTGAATGGCCATTGAGTGTCTTCTCCAAATGGCGAGATCCCA 1297
DB 121 tggatgagtaactgtttctcaggaccttgaggcttcacgtgatcttctcatccca 180
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OY 1298 TGGATGAGTAACTGTTTCTCAGGCACCTTAGGCTTTCATGTAATCTTCTATTACCA 1357
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OY 1358 GTGACTAATTTTCCACAGGCTACTAAAGAACTATGATGTGAGAGAAAGACTAATCATC 1417
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AC W10113;
NT 91284430
DT 29-APR-1996 (Rel. 47, Created)
DE 05-MAR-1997 (Rel. 51, Last updated, Version 2)
DE ma42403.r1 Soares mouse p3JNMF19.5 Mus musculus cDNA clone 313349
5'.
KM EST.
OC Mus musculus (house mouse)
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OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-105
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RA "The WashU-HHMI Mouse EST Project";
RT Unpublished.
RL Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
    Washington University School of Medicine 4444 Forest Park Parkway,
    Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
    Email: mouseest@wustl.edu This clone is available
    royally-free through LNL; contact the IMAGE Consortium
    (info@image.llnl.gov) for further information. Putative full length
    read Seq primer: mob.REGA+ET.
CC Key Location/Qualifiers
FH 1..105
FT source
    1..105
    /organism="Mus musculus"
    /note="Vector: pT73D (Pharmacia) with a modified
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    TGTACCAATCTGAAGTGGAGCGGCGGCGGCGATTTTTTTTTTTTTTTT 3'}.
    double-stranded cDNA was size selected, ligated to Eco RI
    adapters (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of a modified pT73 vector
    (Pharmacia). Library went through one round of
    normalization to a Cot = 5. Library constructed by Bento
    Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr
    Minoru Ko (Wayne State University). "
    /clone="313349"
    /dev_stage="19.5 dpc total fetus"
    /lab_host="DH10B (ampicillin resistant)"
    <1..>105

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SQ Sequence 105 BP; 57 A; 13 C; 21 G; 14 T; 0 other;
Query Match 1..48; Score 21; DB 91; Length 105;
Best Local Similarity 76.9%; Pred. No. 9,46e-03;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
DB 48 aagaagaatgggaataaagaaataaataaataaataa 86
    |||||||
OY 957 AAGAGAAAGTGGAGCAGAACATTTGAAAAAACAATAAA 995

RESULT 6
ID MMA17046 standard; RNA; EST; 107 BP.
AC AA117046;
NT 91672122
DT 17-NOV-1996 (Rel. 49, Created)
DE 18-FEB-1997 (Rel. 51, Last updated, Version 2)
DE mp53f02.r1 Soares 2nbmt Mus musculus cDNA clone 572955 5'.
KM EST.
OC Mus musculus (house mouse)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
RN [1]
RP 1-107
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA Waterston R.;
RA "The WashU-HHMI Mouse EST Project";
RT Unpublished.
RL Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
    Washington University School of Medicine 4444 Forest Park Parkway,
    Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
    Email: mouseest@wustl.edu This clone is available
    royally-free through LNL; contact the IMAGE Consortium
    (info@image.llnl.gov) for further information. MGI:347603 Putative
    full length read vector to vector length is 108 Seq primer: -28M13
    rev2 from Amersham.
CC Key Location/Qualifiers
FH 1..107
FT source
    1..107
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /note="Vector: pT73D-Pac (Pharmacia) with a modified
    polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
    was primed with a Not I - oligo(dT) primer [5',
    TGTACCAATCTGAAGTGGAGCGGCGGCGGCTTTTTTTTTTTTTTTT 3']
    TGTACCAATCTGAAGTGGAGCGGCGGCGGCGGCTTTTTTTTTTTTTTTT 3'}.
    double-stranded cDNA was ligated to Eco RI adapters
    (Pharmacia), digested with Not I and cloned into the Not I
    and Eco RI sites of the modified pT73 vector. RNA provide
    by Dr. Bertrand Jordan. Library went through two rounds of
    normalization, and was constructed by Bento Soares and
    M.Fatima Bonaldo.
    /clone="572955"
    /clone_lib="Soares 2nbmt"
    /sex="male"
    /tissue_type="Thymus"
    /dev_stage="4 weeks"
    /lab_host="DH10B"
    <1..>107
FT mRNA
SQ Sequence 107 BP; 50 A; 16 C; 24 G; 17 T; 0 other;
Query Match 1..48; Score 21; DB 98; Length 107;
Best Local Similarity 76.9%; Pred. No. 9,46e-03;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
DB 65 aagaagaatgggaataaagaaataaataaataaataa 103
    |||||||
OY 957 AAGAGAAAGTGGAGCAGAACATTTGAAAAAACAATAAA 995

```


Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TGTTCAGTCTGTTCTATTTGGA
Primer B: AAAGGAGTCAAAATGGGTTTTC
STS size: 100

PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3

Prepared with primer pairs derived from random genomic sequence.

FEATURES
source
1..245
Location/Qualifiers
/organism="Homo sapiens"

STS
56..155
/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
963_G_6"
56..80
/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
963_G_6"
primer_bind
complement(134..155)
/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
963_G_6"
BASE COUNT 92 a 28 c 35 g 87 t 3 others
ORIGIN

Query Match 1.4%; Score 21; DB 40; Length 245;
Best Local Similarity 70.8%; Pred. No. 9,46e-03;
Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

109 tuctgaatgttaccatttaaaaccatttgacctttt 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
519 TGCATTGATGACGCTCTATTGAGAGACCCATCTGGACATCTTT 472

RESULT 13
LOCUS G06067 253 bp DNA STS 19-OCT-1995
DEFINITION human STS WI-6406.
ACCESSION G06067
NID 9859312
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human STS derived from sequences in dbEST and the Unigene collection.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Channata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Carnivora; Homnidae; Homo.
REFERENCE 1 (bases 1 to 253)
AUTHORS Hudson T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs
JOURNAL Unpublished (1995)
COMMENT Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research

9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: CATTGCTTCATACATACAGTTCC
Primer B: CACACTTGACAGCCGTCGC
STS size: 225

PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3

Prepared with primer pairs derived from Z18433 -- dbEST.

FEATURES
source
1..253
Location/Qualifiers
/organism="Homo sapiens"
STS
29..253
/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage group"
29..53
/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage group"
primer_bind
complement(235..253)
/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage group"
BASE COUNT 76 a 57 c 49 g 70 t 1 others
ORIGIN

Query Match 1.4%; Score 21; DB 38; Length 253;
Best Local Similarity 78.4%; Pred. No. 9,46e-03;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 123 acacagctcacatgtacagacataaaccgtcaag 159
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 774 ACACAGCTCACACAGACAGACTTCAGCTGTCGAG 810

RESULT 14
ID M55835
AC W10583;
NI 91284900
DT 29-APR-1996 (Rel. 47, Created)
DT 03-MAR-1997 (Rel. 51, Last updated, Version 2)
DE m38f10.r1 Soares mouse p1NMF19.5 Mus musculus cDNA clone 313003 5'
DE similar to gp:219554 VIMENTIN (HUMAN);.
KW Est.
OS Mus musculus (house mouse)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
OC [1]
RN 1-267
RP 1-267
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Scheilenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R., Waterston R.;

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RT      "The WashU-HHMI Mouse EST Project";
RL      Unpublished.
CC      Contact: Maria M/Mouse EST Project WashU-HHMI Mouse EST Project
CC      Washington University School of Medicine 4444 Forest Park Parkway,
CC      Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC      Email: mouseest@wustl.wustl.edu This clone is available
CC      royally-free through LNLN; contact the IMAGE Consortium
CC      (info@image.lnl.gov) for further information. Putative full length
CC      read Seq primer: ETP1mer.
FH      Key      Location/Qualifiers
FH      source      1..267
FH      FT      /organism="Mus musculus"
FH      FT      /note="Vector: pT73D (Pharmacia) with a modified
FH      FT      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FH      FT      was primed with a Not I - oligo(dT) primer (5'
FH      FT      TGTTCACATCTGAGTGGAGCGCGCGCATTTTCTTTTCTTTT 3')
FH      FT      double-stranded cDNA was size selected, ligated to Eco RI
FH      FT      adapters (Pharmacia), digested with Not I and cloned into
FH      FT      the Not I and Eco RI sites of a modified pT73 vector
FH      FT      (Pharmacia). Library went through one round of
FH      FT      normalization to a Cot = 5. Library constructed by Bento
FH      FT      Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr
FH      FT      Minoru Ko (Wayne State University)."
FH      FT      /clone_lib="Soares mouse p3NMFL19.5"
FH      FT      /dev_stage="19.5 dpc total fetus"
FH      FT      /lab_host="DH10B (ampicillin resistant)"
FH      FT      <1..>267
FH      FT      mRNA
FH      FT      Sequence 267 BP: 78 A; 70 C; 61 G; 58 T; 0 other;
SQ
Query Match      1.4%; Score 22; DB 95; Length 267;
Best Local Similarity 75.0%; Pred. No. 5.47e-04;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
DB      31 gaagcctcgtggaagcagagagacatctctgcctctgc 74
CP      931 GAAAGCTGCTCGAAGAGTGAGGTTGACATGTCCATGTGCCCTGC 888

RESULT 15
ID      MM157384 standard; RNA; EST; 281 BP.
AC      AA239461;
NT      G1863675
DT      06-MAR-1997 (Rel. 51, Created)
DT      15-MAR-1997 (Rel. 51, Last updated, Version 2)
PF      mv25d08.r1 GuayWoodford Beiler mouse kidney day 0 Mus musculus cDNA
       clone 656079 5' similar to TR:G497940 G497940 MAJOR VAVLT PROTEIN.
       :
km      EST.
OS      Mus musculus (house mouse)
OC      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC      Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC      Mus.
RN      [1]
RP      1-281
RA      Maira M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA      Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA      Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA      Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA      Waterston R.,
RT      "The WashU-HHMI Mouse EST Project";
RL      Unpublished.
CC      Contact: Maria M/Mouse EST Project WashU-HHMI Mouse EST Project
CC      Washington University School of Medicine 4444 Forest Park Parkway,
CC      Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC      Email: mouseest@wustl.wustl.edu This clone is available
CC      royally-free through LNLN; contact the IMAGE Consortium
CC      (info@image.lnl.gov) for further information. MGI:401927 Putative
CC      full length read vector to vector length is 295 Seq primer: -28m13
CC      rev1 ET from Amerham High quality sequence stop: 272.
FH      Key      Location/Qualifiers

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FH      source      1..281
FH      FT      /organism="Mus musculus"
FH      FT      /strain="C57BL/6J"
FH      FT      /note="Vector: pluescript SK-; Site_1: EcoRI; Site_2:
FH      FT      XhoI; Cloned unidirectionally. Primer: Oligo dT. Average
FH      FT      insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
FH      FT      sequence: 5' GAATTCGCGACGAC 3' -3' adaptor sequence: 5'
FH      FT      CTCGAGTTTCTTTTCTTTTCTTTT3' Library provided Lisa
FH      FT      Guay-Woodford."
FH      FT      /clone_lib="GuayWoodford Beiler mouse kidney day 0"
FH      FT      /dev_stage="newborn (day 0)"
FH      FT      /lab_host="SOLR (kanamycin resistant)"
FH      FT      <1..>281
FH      FT      mRNA
FH      FT      Sequence 281 BP: 69 A; 75 C; 90 G; 47 T; 0 other;
SQ
Query Match      1.4%; Score 22; DB 92; Length 281;
Best Local Similarity 80.6%; Pred. No. 5.47e-04;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
DB      148 tgggccccgaaccatcagggacttgctgtgctg 183
CP      43 TGGTCCCGGAAACCTCAGGGGCTTGAGCGCGCG 8

Search completed: Thu Aug 21 10:48:17 1997
Job time : 773 secs.

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